**Amendments to the Specification:**

Please replace paragraph **[0016]** beginning at page 4, line 14, with the following:

--**[0016]** Based on the crystallographic structure of PE (Allured, V.S., et al., *Proc Natl Acad Sci U S A*, 83(5):1320-4 (1986)) and many functional studies, BL22 is thought to kill target cells in the circulation by the following steps. First, in the circulation, the carboxy terminal lysine residue is removed (Hessler, J.L., et al., *Biochemistry*, 36(47):14577-82 (1997)). Next, the Fv portion of the immunotoxin binds to CD22 on the surface of the target cell, and the molecule is internalized into the endocytic compartment, where the protease furin cleaves the toxin between amino acids 279 and 280 of PE (Chiron, M.F., et al., *J Biol Chem*, 269(27):18167-76 (1994); Ogata, M., et al., *J Biol Chem*, 265(33):20678-85 (1990)). Subsequently, the disulfide bond linking cysteines at positions 265 and 287 is reduced producing two fragments. Then the REDL (SEQ ID NO:6) sequence on the carboxyl terminal fragment binds to the KDEL (SEQ ID NO:5) recycling receptor and the fragment containing part of domain 2 and all of domain 3 is transported from the trans-reticular Golgi to the endoplasmic reticulum (ER) (Kreitman, R.J., et al., *Semin Cancer Biol*, 6(5):297-306 (1995)). Once there, amino acids 280-313 somehow facilitate translocation of the toxin into the cytosol, probably taking advantage of preexisting pores in the ER (Theuer, C.P., et al., *Proc Natl Acad Sci U S A*, 90(16):7774-8 (1993); Theuer, C., et al., *Biochemistry*, 33(19):5894-900 (1994)). In the cytosol, the ADP ribosylation activity located within domain III of PE catalytically inactivates elongation factor 2, inhibiting protein synthesis and leading to cell death.--

Please replace paragraph **[0019]** beginning at page 5, line 12, with the following:

--**[0019]** The antibody can further compre a variable heavy (VH) chain comprising three complementarity determining regions (CDRs) designated in order from the CDR closest to the

amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some embodiments, the CDR3 has the sequence of SEQ ID NO:16. In some embodiments, the VH chain has the sequence of SEQ ID NO:21. The antibody can be, for example, an scFv, a dsFv, a Fab, or a F(ab')2.--

Please replace paragraph **[0020]** beginning at page 5, line 20, with the following:

--**[0020]** In another group of embodiments, the invention provides chimeric molecules comprising (a) an antibody that specifically binds CD22, which antibody has a variable light (VL) chain comprising three complementarity determining regions (CDRs) designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, wherein the CDR1 has a sequence selected from the group consisting of SEQ ID NOs:7, 8, 9, and 10; and (b) a therapeutic moiety or a detectable label. The therapeutic moiety or a detectable label can be conjugated or fused to the antibody. In some embodiments, the CDR2 of the chimeric molecule has the sequence of SEQ ID NO:11, and the CDR3 has the sequence of SEQ ID NO:12. The antibody portion of the chimeric molecule can further comprise a variable heavy (VH) chain comprising three complementarity determining regions (CDRs) designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR 2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some embodiments, the VL chain has the sequence of SEQ ID NO:20 and the VH chain has the sequence of SEQ ID NO:21. The therapeutic moiety can be, for example, a cytotoxin, a drug, a radioisotope, or a liposome loaded with a drug or a cytotoxin. In some embodiments, the therapeutic moiety is a cytotoxin is selected from the group consisting of ricin A, abrin, ribotoxin, ribonuclease, saporin, calicheamycin, diphtheria toxin, or a cytotoxic fragment or mutant thereof, *Pseudomonas*

exotoxin A or a cytotoxic fragment or mutant thereof ("PE"), or botulinum toxin A through F. In some embodiments, the PE is selected from the group consisting of PE35, PE38, PE38KDEL, PE40, PE4E, and PE38QQR. In some embodiments, the PE has a substituent of glycine, alanine, valine, leucine, or isoleucine in place of arginine at the position corresponding to position 490 of SEQ ID NO:24. In a preferred embodiment, the substituent at position 490 is alanine.--

Please replace paragraph **[0022]** beginning at page 6, line 15, with the following:

--**[0022]** In yet another group of embodiments, the invention provides for the use of an antibody that specifically binds CD22, the anti-CD22 antibody having a variable light (VL) chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus as CDRs 1, 2, and 3, respectively, wherein CDR1 has a sequence selected from the group consisting of SEQ ID NOs:7, 8, 9, and 10, for the manufacture of a medicament to inhibit the growth of a CD22+ cancer cell. In some embodiments, the CDR 2 has the sequence of SEQ ID NO:11, and the CDR3 has the sequence of SEQ ID NO:12. The antibody can further comprise a variable heavy (VH) chain comprising three complementarity determining regions (CDRs), the CDRs being designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus as CDRs 1, 2, and 3, respectively, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR 2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some embodiments, the VL chain has the sequence of SEQ ID NO:20 and said VH chain has the sequence of SEQ ID NO:21. The antibody can be, for example, an scFv, dsFv, a Fab, or a F(ab')2. The antibody can be attached to a therapeutic moiety or a detectable label. Where the antibody is attached to a therapeutic moiety, the therapeutic moiety can be, for example, a cytotoxin, a drug, a radioisotope, or a liposome loaded with a drug or a cytotoxin. In some preferred embodiments, the therapeutic moiety is a cytotoxin. In some embodiments, the cytotoxin is selected from the group consisting of ricin A, abrin, ribotoxin, ribonuclease, saporin,

calicheamycin, diphtheria toxin or a cytotoxic fragment or mutant thereof, a Pseudomonas exotoxin A or a cytotoxic fragment or mutant thereof ("PE"), and botulinum toxins A through F. Where the cytotoxin is PE, the PE can be, for example, PE35, PE38, PE38KDEL, PE40, PE4E, or PE38QQR. In some preferred embodiments, the PE has a glycine, alanine, valine, leucine, or isoleucine in place of arginine at the position corresponding to position 490 of SEQ ID NO:24. In a preferred embodiment, alanine is substituted for arginine at position 490.--

Please replace paragraph **[0023]** beginning at page 7, line 10, with the following:

--**[0023]** In still another group of embodiments, the invention provides isolated nucleic acids encoding a variable light (VL) chain comprising three complementarity determining regions (CDRs), the CDRs being designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus as CDRs 1, 2, and 3, respectively, wherein the CDR1 has a sequence selected from the group consisting of SEQ ID NOs:7, 8, 9, and 10. In some embodiments, the CDR 2 has the sequence of SEQ ID NO:11, and the CDR3 has the sequence of SEQ ID NO:12. The nucleic acids can further encode a variable heavy (VH) chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, respectively, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR 2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some embodiments the VL chain has the sequence of SEQ ID NO:20 and the VH chain of said encoded antibody has the sequence of SEQ ID NO:21. In some embodiments, the nucleic acid encodes an antibody selected from the group consisting of an scFv, a dsFv, a Fab, or a F(ab')2. In some embodiments, the nucleic acid further encodes a polypeptide which is a therapeutic moiety or a detectable label. Where the nucleic acid encodes a therapeutic moiety, the moiety can be, for example, a drug or a cytotoxin. Where it is a cytotoxin, it can be, for example, *Pseudomonas* exotoxin A or a cytotoxic fragment or mutant thereof ("PE"). The PE can be, for example, PE35, PE38, PE38KDEL, PE40, PE4E,

or PE38QQR. In some embodiments, the PE has a glycine, alanine, valine, leucine, or isoleucine in place of arginine at the position corresponding to position 490 of SEQ ID NO:24. In preferred embodiments, alanine is substituted for arginine at position 490.--

Please replace paragraph **[0025]** beginning at page 8, line 4, with the following:

--**[0025]** In another group of embodiments, the invention provides methods of inhibiting growth of a CD22+ cancer cell by contacting said cell with a chimeric molecule comprising (a) an antibody that binds to CD22, the antibody having a variable light (VL) chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, respectively, wherein the CDR1 has a sequence selected from the group consisting of SEQ ID NOs:7, 8, 9, and 10, and (b) a therapeutic moiety, wherein the therapeutic moiety inhibits the growth of said cell. In some embodiments, the CDR 2 of said VL has the sequence of SEQ ID NO:11, and the CDR3 of said VL has the sequence of SEQ ID NO:12. In some embodiments, the antibody comprises a VH chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, respectively, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR 2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some of the methods, the VL chain has the sequence of SEQ ID NO:20 and said VH chain has the sequence of SEQ ID NO:21. The antibody can be, for example, an scFv, a dsFv, a Fab, or a F(ab')2. The therapeutic moiety can be, for example, a cytotoxin, a drug, a radioisotope, or a liposome loaded with a drug or a cytotoxin. Where the therapeutic moiety is a cytotoxin, the cytotoxin can be, for example, ricin A, abrin, ribotoxin, ribonuclease, saporin, calicheamycin, diphtheria toxin or a cytotoxic fragment or mutant thereof, *Pseudomonas* exotoxin A or a cytotoxic fragment or mutant thereof ("PE"), or botulinum toxin A through F. The PE can be, for example, consisting of PE35, PE38, PE38KDEL, PE40, PE4E, and PE38QQR. Where the

cytotoxin is PE, the PE can have a glycine, alanine, valine, leucine, or isoleucine in place of arginine at the position corresponding to position 490 of SEQ ID NO:24. In a preferred embodiment, alanine is substituted for arginine at a position corresponding to position 490 of SEQ ID NO:24.--

Please replace paragraph **[0026]** beginning at page 8, line 30, with the following:

--**[0026]** In yet another group of embodiments, the invention provides methods for detecting the presence of a CD22+ cancer cell in a biological sample. The methods comprise (a) contacting cells of the biological sample with a chimeric molecule comprising (i) an antibody that specifically binds to CD22, the antibody having a variable light (VL) chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, respectively, wherein the CDR1 has a sequence selected from the group consisting of SEQ ID NOs:7, 8, 9, and 10, conjugated or fused to (ii) a detectable label; and, (b) detecting the presence or absence of said label, wherein detecting the presence of said label indicates the presence of a CD22+ cancer cell in said sample. In some embodiments, the CDR 2 of said VL of said antibody has the sequence of SEQ ID NO:11, and the CDR3 of the VL of said antibody has the sequence of SEQ ID NO:12. In some embodiments, the antibody further comprises a variable heavy (VH) chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, respectively, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR 2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some embodiments, the VL chain has the sequence of SEQ ID NO:20 and the VH chain has the sequence of SEQ ID NO:21. The antibody can be, for example, an scFv, a dsFv, a Fab, or a F(ab')2.--

Please replace paragraph **[0027]** beginning at page 9, line 17, with the following:

--**[0027]** In yet another group of embodiments, the invention provides kits. The kits comprise (a) a container, and (b) a chimeric molecule comprising (i) an anti-CD22 antibody having a variable light (VL) chain comprising three complementarity determining regions (CDRs), the CDRs designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, respectively, wherein the CDR1 has a sequence selected from the group consisting of SEQ ID NOs:7, 8, 9, and 10, conjugated or fused to (ii) a detectable label or a therapeutic moiety. In some embodiments, the CDR 2 of the VL of the antibody has the sequence of SEQ ID NO:11, and the CDR3 of the VL of the antibody has the sequence of SEQ ID NO:12. In some embodiments, the antibody further comprises a variable heavy (VH) chain comprising three complementarity determining regions (CDRs) designated in order from the CDR closest to the amino terminus to the CDR closest to the carboxyl terminus CDRs 1, 2, and 3, wherein the CDR1 has the sequence of SEQ ID NO:13, the CDR 2 has the sequence of ~~SEQ ID NO:15~~ SEQ ID NO:14, and the CDR3 has a sequence selected from the group consisting of SEQ ID NOs:15, 16, 17, 18, and 19. In some embodiments, the VL chain has the sequence of SEQ ID NO:20 and the VH chain has the sequence of SEQ ID NO:21. The antibody can be, for example, an scFv, a dsFv, a Fab, or a F(ab')2. The therapeutic moiety can be, for example, a cytotoxin, a drug, a radioisotope, or a liposome loaded with a drug or a cytotoxin.--

Please replace paragraph **[0035]** beginning at page 11, line 24, with the following:

--**[0035] Figure 1**. Figure 1 sets forth the nucleotide sequence ~~(SEQ ID NO:3)~~ (SEQ ID NO:1) and amino acid sequence ~~(SEQ ID NO:4)~~ (SEQ ID NO:2) of the variable region of the RFB4 light chain and the nucleotide sequence ~~(SEQ ID NO:1)~~ (SEQ ID NO:3) and amino acid sequence ~~(SEQ ID NO:2)~~ (SEQ ID NO:4) of the variable region of the RFB4 heavy chain. The CDRs assigned using the IMGT program (Lefranc, *Nucl. Acids Res.* 29:207-209, 2001; also found on-line by entering "http://", followed by "imgt.cines.fr") are underlined (~~while~~ While not

numbered, CDRs 1, 2 and 3 of each chain are presented within their respective chain in increasing numerical order. For example, CDR2 of the VH chain (SEQ ID NO:14 is the second region underlined in the VH chain.). DNA hot spots (A/G-G-C/T-A/T and A-G-C/T) are highlighted.--

Please replace paragraph **[0036]** beginning at page 12, line 1, with the following:

--**[0036] Figure 2**. Figure 2 is a print out of Entry Number 038145 of the Kabat database showing the nucleic acid (SEQ ID NO:1) and amino acid sequence ~~(SEQ NO:4)~~ (SEQ ID NO:2) of the variable region of the RFB4 light chain and the Kabat position numbering corresponding to each amino acid residue.--

Please replace paragraph **[0037]** beginning at page 12, line 4, with the following:

--**[0037] Figure 3**. Figure 3 is a print out of Entry Number 038146 of the Kabat database showing the nucleic acid (SEQ ID NO:3) and amino acid sequence ~~(SEQ NO:2)~~ (SEQ ID NO:4) of the variable region of the RFB4 heavy chain and the Kabat position numbering corresponding to each amino acid residue.--

Please replace paragraph **[0050]** beginning at page 15, line 1, with the following:

--**[0050]** The amino acid sequence of the RFB4 $V_L$ chain ~~(SEQ ID NO:4)~~ (SEQ ID NO:2), and the Kabat and Wu numbering for each residue in the chain, is shown in Figure 2 (the Kabat and Wu number for each residue is set forth in the second of the two vertical columns of numbers).--

Please replace paragraph **[0053]** beginning at page 15, line 18, with the following:

--**[0053]** The L-CDR1 mutants set forth above can be substituted into the native sequence of the RFB4 light chain ~~(SEQ ID NO:4)~~ (SEQ ID NO:2), in combination with a RFB4 heavy chain of native sequence ~~(SEQ ID NO:2)~~ (SEQ ID NO:4) to create antibodies of higher affinity for CD22 than parental antibody RFB4. Preferably, the L-CDR1 mutations set forth above are used in a RFB4 light chain in combination with one of the four H-CDR3 mutants described above, in which the native sequence SSY at positions 100, 100A and 100B of H-CDR3 is mutated to one of the following four sequences: THW, YNW, TTW, and STY. More preferably, the L-CDR1 mutants described above are used in a RFB4 light chain in combination with a RFB4 heavy chain in which the native sequence SSY at positions 100, 100A and 100B of H-CDR3 is mutated to THW.--

Please replace paragraph **[0077]** beginning at page 22, line 11, with the following:

--**[0077]** "RFB4" refers to a mouse IgG1 monoclonal antibody that specifically binds to human CD22. RFB4 is commercially available under the name RFB4 from several sources, such as Southern Biotechnology Associates, Inc. (Birmingham AL; Cat. No. 9360-01), Autogen Bioclear UK Ltd. (Calne, Wilts, UK; Cat. No. AB147), Axxora LLC. (San Diego, CA). RFB4 is highly specific for cells of the B lineage and has no detectable cross-reactivity with other normal cell types. Li et al., Cell. Immunol. 118:85-99 (1989). The heavy and light chains of RFB4 have been cloned. See, Mansfield et al., Blood 90:2020-2026 (1997), which is incorporated herein by reference. The nucleotide sequence and amino acid sequences of the RFB4 ~~heavy~~ light chain are SEQ ID NO:1 and SEQ ID NO:2, respectively. The nucleotide sequence and amino acid sequences of the RFB4 ~~light~~ heavy chain are SEQ ID NO:3 and SEQ ID NO:4, respectively. The sequences of each chain are set forth in Figure 1.--

Please replace paragraph **[0130]** beginning at page 34, line 26, with the following:

--**[0130]** The positions of amino acid residues in an antibody heavy chain or light chain are conveniently referred to in the art by standard numbering as set forth in Kabat, E., *et al.*, SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST, U.S. Government Printing Office, NIH Publication No. 91-3242 (1991). See also, Johnson, G. and Wu, T., Nuc. Acids Res. 29:205-206 (2001). The Kabat et al. database is typically referred to in the art as either "Kabat" or "Kabat and Wu". The database is currently maintained on-line as a subscription service and can be found by entering "www." followed by "kabatdatabase.com". The heavy and light chains of RFB4 have been cloned. See, Mansfield et al., Blood 90:2020-2026 (1997). The amino acid sequences of the RFB4 $V_L$ and $V_H$ chains and a list of the Kabat numbering of the position of each amino acid residue are set forth in the Kabat database under Entry Numbers 038145 and 038146, respectively. Figure 2 shows the comparison of the numbering of the amino acids of the RFB4 $V_L$ chain ~~(SEQ ID NO:4)~~ (SEQ ID NO:2) to the corresponding Kabat positions as set forth in Kabat Entry 038145; Figure 3 shows the same comparison for the amino acids of the RFB4 $V_H$ chain ~~(SEQ ID NO:2)~~ (SEQ ID NO:4), as set forth in Kabat Entry 038146.--

Please replace paragraph **[0161]** beginning at page 43, line 28, with the following:

--**[0161]** As noted above, some or all of domain 1b may be deleted, and the remaining portions joined by a linker or directly by a peptide bond. Some of the amino portion of domain II may be deleted. And, the C-terminal end may contain the native sequence of residues 609-613 (REDLK ~~(SEQ ID NO:7)~~ (SEQ ID NO:30)), or may contain a variation found to maintain the ability of the construct to translocate into the cytosol, such as REDL (SEQ ID NO:6) or KDEL (SEQ ID NO:5), and repeats of these sequences. See, e.g., U.S. Patents 5,854,044; 5,821,238; and 5,602,095 and WO 99/51643. While in preferred embodiments, the PE is PE4E, PE40, or PE38, any form of PE in which non-specific cytotoxicity has been eliminated or reduced to levels in which significant toxicity to non-targeted cells does not occur can be used in the immunotoxins

of the present invention so long as it remains capable of translocation and EF-2 ribosylation in a targeted cell.--

Please replace paragraph **[0203]** beginning at page 56, line 9, with the following:

--**[0203]** Mutations were introduced using two-step overlap PCR method and the RFB4 ($V_H$-GTHW ~~(SEQ ID NO: )~~ (SEQ ID NO:29)) –PE38 plasmid DNA used as template. Mutagenic primers that contain mutated sites (bold letter) and restriction endonuclease sites of *Sal* I and *Eco*RI (underlined) are as follows: primer A (5'- GAACCCGACGCA**GCC** GGCCGTATCCGCAAC-3' (SEQ ID NO:25), upstream) and primer B (5'-GTTGCGGATA CGGCC**GGC**TGCGTCGGGTTC-3' (SEQ ID NO:26), downstream) and primer C (5'-GCTGTCGTGGAACCAGGTCGACCAGG-3' (SEQ ID NO:27)) and primer D (5'-CTTT GTTAGCAGCCGAATTCATATTCGAT-3' (SEQ ID NO:28)).--

Please cancel the present "SEQUENCE LISTING", pages 1-14, submitted with the instant application on May 25, 2006, as well as the informal "SEQUENCE LISTING", pages 1/7 through 7/7, published with WO 2005/052006, and insert therefor the accompanying paper copy of the enclosed Substitute Sequence Listing, page numbers 1 to 14, at the end of the application.